

SEQUENCE LISTING

<110> Rhône-Poulenc Rorer

<120> MEKK1-interacting FHA protein 1 (MIF1)

<130> sequences

<140>

<141>

<150> 93590

<151> 1998-07-21

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 1553

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (2)..(1174)

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10

15

ccc tcc tcc agt gag aaa aag aag gta tcc aaa gcc ccc agc act cct 97

Pro Ser Ser Ser Glu Lys Lys Lys Val Ser Lys Ala Pro Ser Thr Pro

20

25

30

gtg cca ccc agc cca gcc cca gcc cct gga ctc acc aag cgt gtg aag 145

Val Pro Pro Ser Pro Ala Pro Ala Pro Gly Leu Thr Lys Arg Val Lys

35

40

45

aag agt aaa cag cca ctt cag gtg acc aag gat ctg ggc cgc tgg aag 193

Lys Ser Lys Gln Pro Leu Gln Val Thr Lys Asp Leu Gly Arg Trp Lys

50

55

60

cct gca aat gac ctc ctg ctc ata aat gct gtg ttg cag acc aac gac 241

Pro Ala Asn Asp Leu Leu Leu Ile Asn Ala Val Leu Gln Thr Asn Asp

65	70	75	80	
ctg acc tcc gtc cac	ctg ggc gtg aaa	ttc agc tgc cgc	ttc acc ctt	289
Leu Thr Ser Val His	Leu Gly Val Lys	Phe Ser Cys Arg	Phe Thr Leu	
85	90	95		
cgg gag gtc cag gag	cgt tgg tac gcc	ctg ctc tac gat	cct gtc atc	337
Arg Glu Val Gln Glu	Arg Trp Tyr Ala	Leu Leu Tyr Asp	Pro Val Ile	
100	105	110		
tcc aag ttg gcc tgt	cag gcc atg agg	cag ctg cac cca	gag gct att	385
Ser Lys Leu Ala Cys	Gln Ala Met Arg	Gln Leu His Pro	Glu Ala Ile	
115	120	125		
gca gcc atc cag agc	aag gcc ctg ttt	agc aag gct gag	gag cag ctg	433
Ala Ala Ile Gln Ser	Lys Ala Leu Phe	Ser Lys Ala Glu	Glu Gln Leu	
130	135	140		
ctg agc aaa gtg gga	tcg acc agc cag	ccc acc ttg gag	acc ttc cag	481
Leu Ser Lys Val Gly	Ser Thr Ser Gln	Pro Thr Leu Glu	Thr Phe Gln	
145	150	155	160	
gac ctg ctg cac aga	cac cct gat gcc	ttc tac ctg gcc	cgt acc gcg	529
Asp Leu Leu His Arg	His Pro Asp Ala	Phe Tyr Leu Ala	Arg Thr Ala	
165	170	175		
aag gcc ctg cag gcc	cac tgg cag ctc	atg aag cag tat	tac ctg ctg	577
Lys Ala Leu Gln Ala	His Trp Gln Leu	Met Lys Gln Tyr	Tyr Leu Leu	
180	185	190		
gag gac cag aca gtg	cag ccg ctg ccc	aaa ggg gac caa	gtg ctg aac	625
Glu Asp Gln Thr Val	Gln Pro Leu Pro	Lys Gly Asp Gln	Val Leu Asn	
195	200	205		
ttc tct gat gca gag	gac ctg att gat	gac agt aag ctc	aag gac atg	673
Phe Ser Asp Ala Glu	Asp Leu Ile Asp	Asp Ser Lys Leu	Lys Asp Met	
210	215	220		
cga gat gag gtc ctg	gaa cat gag ctg	atg gtg gct gac	cgg cgc cag	721
Arg Asp Glu Val Leu	Glu His Glu Leu	Met Val Ala Asp	Arg Arg Gln	
225	230	235	240	
aag cga gag att cgg	cag ctg gaa cag	gaa ctg cat aag	tgg cag gtg	769
Lys Arg Glu Ile Arg	Gln Leu Glu Gln	Glu Leu His Lys	Trp Gln Val	
245	250	255		

cta gtg gac agc atc aca ggc atg agc tct ccg gac ttc gac aac cag 817
 Leu Val Asp Ser Ile Thr Gly Met Ser Ser Pro Asp Phe Asp Asn Gln
 260 265 270

aca ctg gca gtg ctg cgg ggc cgc atg gtg cgg tac ctg atg cgc tcg 865
 Thr Leu Ala Val Leu Arg Gly Arg Met Val Arg Tyr Leu Met Arg Ser
 275 280 285

cgt gag atc acc ctg ggc aga gca acc aag gat aac cag att gat gtg 913
 Arg Glu Ile Thr Leu Gly Arg Ala Thr Lys Asp Asn Gln Ile Asp Val
 290 295 300

gac ctg tct ctg gag ggt ccg gcc tgg aag ata tcc cgg aaa caa ggt 961
 Asp Leu Ser Leu Glu Gly Pro Ala Trp Lys Ile Ser Arg Lys Gln Gly
 305 310 315 320

gtc atc aag ctg aag aac aac ggt gat ttc ttc att gcc aat gag ggt 1009
 Val Ile Lys Leu Lys Asn Asn Gly Asp Phe Phe Ile Ala Asn Glu Gly
 325 330 335

cga cgg ccc atc tac atc gat gga cgg ccg gtg ctc tgt ggc tcc aaa 1057
 Arg Arg Pro Ile Tyr Ile Asp Gly Arg Pro Val Leu Cys Gly Ser Lys
 340 345 350

tgg cgc ctc agc aac aac tct gtg gtg gag atc gcc agc ctg cga ttc 1105
 Trp Arg Leu Ser Asn Asn Ser Val Val Glu Ile Ala Ser Leu Arg Phe
 355 360 365

gtc ttc ctt atc aac cag gac ctc att gcc ctc atc agg gct gag gct 1153
 Val Phe Leu Ile Asn Gln Asp Leu Ile Ala Leu Ile Arg Ala Glu Ala
 370 375 380

gcc aag atc aca cca cag tga ggaatggtgg caggactcgt gggccctctc 1204
 Ala Lys Ile Thr Pro Gln
 385 390

cggcctgttt cccctgccac tccagccccc ttgagctggg aactcaggct cctggaaaaa 1264

cctgggcagt gggaggctca gctgcggggc attgatttga gcctttgagg gaggataggg 1324

ctggcctttg tgaagccagc agaggctgag aacctcaggc ttccctagat ccagagcccc 1384

tccccatctt cctctctcta aaaacaaccc tccccccat tctaccccc atfgccacct 1444

tcactcctgt gtctccagct gattagcctc agactcttct tttattgttt ttcttttgta 1504

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1553

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<211> 390

<212> PRT

<213> homo sapiens

<400> 2

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15

Pro Ser Ser Ser Glu Lys Lys Lys Val Ser Lys Ala Pro Ser Thr Pro

20

25

30

Val Pro Pro Ser Pro Ala Pro Ala Pro Gly Leu Thr Lys Arg Val Lys

35

40

45

Lys Ser Lys Gln Pro Leu Gln Val Thr Lys Asp Leu Gly Arg Trp Lys

50

55

60

Pro Ala Asn Asp Leu Leu Leu Ile Asn Ala Val Leu Gln Thr Asn Asp

65

70

75

80

Leu Thr Ser Val His Leu Gly Val Lys Phe Ser Cys Arg Phe Thr Leu

85

90

95

Arg Glu Val Gln Glu Arg Trp Tyr Ala Leu Leu Tyr Asp Pro Val Ile

100

105

110

Ser Lys Leu Ala Cys Gln Ala Met Arg Gln Leu His Pro Glu Ala Ile

115

120

125

Ala Ala Ile Gln Ser Lys Ala Leu Phe Ser Lys Ala Glu Glu Gln Leu

130

135

140

Leu Ser Lys Val Gly Ser Thr Ser Gln Pro Thr Leu Glu Thr Phe Gln

145

150

155

160

Asp Leu Leu His Arg His Pro Asp Ala Phe Tyr Leu Ala Arg Thr Ala

165

170

175

Lys Ala Leu Gln Ala His Trp Gln Leu Met Lys Gln Tyr Tyr Leu Leu

180

185

190

Glu Asp Gln Thr Val Gln Pro Leu Pro Lys Gly Asp Gln Val Leu Asn

195	200	205
Phe Ser Asp Ala Glu Asp Leu Ile Asp Asp Ser Lys Leu Lys Asp Met		
210	215	220
Arg Asp Glu Val Leu Glu His Glu Leu Met Val Ala Asp Arg Arg Gln		
225	230	235 240
Lys Arg Glu Ile Arg Gln Leu Glu Gln Glu Leu His Lys Trp Gln Val		
	245	250 255
Leu Val Asp Ser Ile Thr Gly Met Ser Ser Pro Asp Phe Asp Asn Gln		
	260	265 270
Thr Leu Ala Val Leu Arg Gly Arg Met Val Arg Tyr Leu Met Arg Ser		
	275	280 285
Arg Glu Ile Thr Leu Gly Arg Ala Thr Lys Asp Asn Gln Ile Asp Val		
	290	295 300
Asp Leu Ser Leu Glu Gly Pro Ala Trp Lys Ile Ser Arg Lys Gln Gly		
305	310	315 320
Val Ile Lys Leu Lys Asn Asn Gly Asp Phe Phe Ile Ala Asn Glu Gly		
	325	330 335
Arg Arg Pro Ile Tyr Ile Asp Gly Arg Pro Val Leu Cys Gly Ser Lys		
	340	345 350
Trp Arg Leu Ser Asn Asn Ser Val Val Glu Ile Ala Ser Leu Arg Phe		
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Val Phe Leu Ile Asn Gln Asp Leu Ile Ala Leu Ile Arg Ala Glu Ala		
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Ala Lys Ile Thr Pro Gln		
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 <212> DNA
 <213> Artificial Sequence
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<223> Description of Artificial Sequence:
oligonucleotide

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<210> 4

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
oligonucleotide

<400> 4

cgggatccat ggacaaagat tctcag 26

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<211> 53

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
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<211> 53

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
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<210> 7
<211> 1914
<212> DNA
<213> homo sapiens
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accagtggct ttgggactgt aagagg atg gac aaa gat tct cag ggg ctg cta 173
Met Asp Lys Asp Ser Gln Gly Leu Leu
1 5

gat tca tcc ctg atg gca tca ggc act gcc agc cgc tca gag gat gag 221
Asp Ser Ser Leu Met Ala Ser Gly Thr Ala Ser Arg Ser Glu Asp Glu
10 15 20 25

gag tca ctg gca ggg cag aag cga gcc tcc tcc cag gcc ttg ggc acc 269
Glu Ser Leu Ala Gly Gln Lys Arg Ala Ser Ser Gln Ala Leu Gly Thr
30 35 40

atc cct aaa cgg aga agc tcc tcc agg ttc atc aag agg aag aag ttc 317
Ile Pro Lys Arg Arg Ser Ser Ser Arg Phe Ile Lys Arg Lys Lys Phe
45 50 55

gat gat gag ctg gtg gag agc agc ctg gca aaa tct tct acc cgg gca 365
Asp Asp Glu Leu Val Glu Ser Ser Leu Ala Lys Ser Ser Thr Arg Ala
60 65 70

aag ggg gcc agt ggg gtg gaa cca ggg cgc tgt tcg ggg agt gaa ccc 413
Lys Gly Ala Ser Gly Val Glu Pro Gly Arg Cys Ser Gly Ser Glu Pro
75 80 85

tcc tcc agt gag aag aag aag gta tcc aaa gcc ccc agc act cct gtg 461
Ser Ser Ser Glu Lys Lys Lys Val Ser Lys Ala Pro Ser Thr Pro Val
90 95 100 105

cca ccc agc cca gcc cca gcc cct gga ctc acc aag cgt gtg aag aag 509
Pro Pro Ser Pro Ala Pro Ala Pro Gly Leu Thr Lys Arg Val Lys Lys
110 115 120

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agt aaa cag cca ctt cag gtg acc aag gat ctg ggc cgc tgg aag cct	557
Ser Lys Gln Pro Leu Gln Val Thr Lys Asp Leu Gly Arg Trp Lys Pro	
125 130 135	
gca gat gac ctc ctg ctc ata aat gct gtg ttg cag acc aac gac ctg	605
Ala Asp Asp Leu Leu Leu Ile Asn Ala Val Leu Gln Thr Asn Asp Leu	
140 145 150	
acc tcc gtc cac ctg ggc gtg aaa ttc agc tgc cgc ttc acc ctt cgg	653
Thr Ser Val His Leu Gly Val Lys Phe Ser Cys Arg Phe Thr Leu Arg	
155 160 165	
gag gtc cag gag cgt tgg tac gcc ctg ctc tac gat cct gtc atc tcc	701
Glu Val Gln Glu Arg Trp Tyr Ala Leu Leu Tyr Asp Pro Val Ile Ser	
170 175 180 185	
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Lys Leu Ala Cys Gln Ala Met Arg Gln Leu His Pro Glu Ala Ile Ala	
190 195 200	
gcc atc cag agc aag gcc ctg ttt agc aag gct gag gag cag ctg ctg	797
Ala Ile Gln Ser Lys Ala Leu Phe Ser Lys Ala Glu Glu Gln Leu Leu	
205 210 215	
agc aaa gtg gga tcg acc agc cag ccc acc ttg gag acc ttc cag gac	845
Ser Lys Val Gly Ser Thr Ser Gln Pro Thr Leu Glu Thr Phe Gln Asp	
220 225 230	
ctg ctg cac aga cac cct gat gcc ttc tac ctg gcc cgt acc gcg aag	893
Leu Leu His Arg His Pro Asp Ala Phe Tyr Leu Ala Arg Thr Ala Lys	
235 240 245	
gcc ctg cag gcc cac tgg cag ctc atg aag cag tat tac ctg ctg gag	941
Ala Leu Gln Ala His Trp Gln Leu Met Lys Gln Tyr Tyr Leu Leu Glu	
250 255 260 265	
gac cag aca gtg cag ccg ctg ccc aaa ggg gac caa gtg ctg aac ttc	989
Asp Gln Thr Val Gln Pro Leu Pro Lys Gly Asp Gln Val Leu Asn Phe	
270 275 280	
tct gat gca gag gac ctg att gat gac agt aag ctc aag gac atg cga	1037
Ser Asp Ala Glu Asp Leu Ile Asp Asp Ser Lys Leu Lys Asp Met Arg	
285 290 295	
gat gag gtc ctg gaa cat gag ctg atg gtg gct gac cgg cgc cag aag	1085
Asp Glu Val Leu Glu His Glu Leu Met Val Ala Asp Arg Arg Gln Lys	

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cga gag att cgg cag ctg gaa cag gaa ctg cat aag tgg cag gtg cta			1133
Arg Glu Ile Arg Gln Leu Glu Gln Glu Leu His Lys Trp Gln Val Leu			
315	320	325	
gtg gac agc atc aca ggc atg agc tct ccg gac ttc gac aac cag aca			1181
Val Asp Ser Ile Thr Gly Met Ser Ser Pro Asp Phe Asp Asn Gln Thr			
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ctg gca gtg ctg cgg ggc cgc atg gtg cgg tac ctg atg cgc tcg cgt			1229
Leu Ala Val Leu Arg Gly Arg Met Val Arg Tyr Leu Met Arg Ser Arg			
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gag atc acc ctg ggc aga gca acc aag gat aac cag att gat gtg gac			1277
Glu Ile Thr Leu Gly Arg Ala Thr Lys Asp Asn Gln Ile Asp Val Asp			
365	370	375	
ctg tct ctg gag ggt ccg gcc tgg aag ata tcc cgg aaa caa ggt gtc			1325
Leu Ser Leu Glu Gly Pro Ala Trp Lys Ile Ser Arg Lys Gln Gly Val			
380	385	390	
atc aag ctg aag aac aac ggt gat ttc ttc att gcc aat gag ggt cga			1373
Ile Lys Leu Lys Asn Asn Gly Asp Phe Phe Ile Ala Asn Glu Gly Arg			
395	400	405	
cgg ccc atc tac atc gat gga cgg ccg gtg ctc tgt ggc tcc aaa tgg			1421
Arg Pro Ile Tyr Ile Asp Gly Arg Pro Val Leu Cys Gly Ser Lys Trp			
410	415	420	425
cgc ctc agc aac aac tct gtg gtg gag atc gcc agc ctg cga ttc gtc			1469
Arg Leu Ser Asn Asn Ser Val Val Glu Ile Ala Ser Leu Arg Phe Val			
430	435	440	
ttc ctt atc aac cag gac ctc att gcc ctc atc agg gct gag gct gcc			1517
Phe Leu Ile Asn Gln Asp Leu Ile Ala Leu Ile Arg Ala Glu Ala Ala			
445	450	455	
aag atc aca cca cag tga ggaatggtgg caggactcgt gggccctctc			1565
Lys ile Thr Pro Gln			
460			
cggcctgttt cccctgccac tccagccccc ttgagctggg aactcaggct cctggaaaaa			1625
cctgggacagt gggaggctca gctgcgggcc attgatttga gcctttgagg gaggataggg			1685

ctggcctttg tgaagccagc agaggctgag aacctcaggc ttccctagat ccagagcccc 1745
 tccccatctt cctctctcta aaaacaaccc tccccccat tctaccccc attgccacct 1805
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 aataaaaagc accaggttcc aaagtaaaaa aaaaaaaaaa aaactcgag 1914

<210> 8
 <211> 462
 <212> PRT
 <213> homo sapiens

<400> 8

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Arg Ala Ser Ser Gln Ala Leu Gly Thr Ile Pro Lys Arg Arg Ser Ser
 35 40 45

Ser Arg Phe Ile Lys Arg Lys Lys Phe Asp Asp Glu Leu Val Glu Ser
 50 55 60

Ser Leu Ala Lys Ser Ser Thr Arg Ala Lys Gly Ala Ser Gly Val Glu
 65 70 75 80

Pro Gly Arg Cys Ser Gly Ser Glu Pro Ser Ser Ser Glu Lys Lys Lys
 85 90 95

Val Ser Lys Ala Pro Ser Thr Pro Val Pro Pro Ser Pro Ala Pro Ala
 100 105 110

Pro Gly Leu Thr Lys Arg Val Lys Lys Ser Lys Gln Pro Leu Gln Val
 115 120 125

Thr Lys Asp Leu Gly Arg Trp Lys Pro Ala Asp Asp Leu Leu Leu Ile
 130 135 140

Asn Ala Val Leu Gln Thr Asn Asp Leu Thr Ser Val His Leu Gly Val
 145 150 155 160

Lys Phe Ser Cys Arg Phe Thr Leu Arg Glu Val Gln Glu Arg Trp Tyr

165	170	175
Ala Leu Leu Tyr Asp Pro Val Ile Ser Lys Leu Ala Cys Gln Ala Met		
180	185	190
Arg Gln Leu His Pro Glu Ala Ile Ala Ala Ile Gln Ser Lys Ala Leu		
195	200	205
Phe Ser Lys Ala Glu Glu Gln Leu Leu Ser Lys Val Gly Ser Thr Ser		
210	215	220
Gln Pro Thr Leu Glu Thr Phe Gln Asp Leu Leu His Arg His Pro Asp		
225	230	235 240
Ala Phe Tyr Leu Ala Arg Thr Ala Lys Ala Leu Gln Ala His Trp Gln		
245	250	255
Leu Met Lys Gln Tyr Tyr Leu Leu Glu Asp Gln Thr Val Gln Pro Leu		
260	265	270
Pro Lys Gly Asp Gln Val Leu Asn Phe Ser Asp Ala Glu Asp Leu Ile		
275	280	285
Asp Asp Ser Lys Leu Lys Asp Met Arg Asp Glu Val Leu Glu His Glu		
290	295	300
Leu Met Val Ala Asp Arg Arg Gln Lys Arg Glu Ile Arg Gln Leu Glu		
305	310	315 320
Gln Glu Leu His Lys Trp Gln Val Leu Val Asp Ser Ile Thr Gly Met		
325	330	335
Ser Ser Pro Asp Phe Asp Asn Gln Thr Leu Ala Val Leu Arg Gly Arg		
340	345	350
Met Val Arg Tyr Leu Met Arg Ser Arg Glu Ile Thr Leu Gly Arg Ala		
355	360	365
Thr Lys Asp Asn Gln Ile Asp Val Asp Leu Ser Leu Glu Gly Pro Ala		
370	375	380
Trp Lys Ile Ser Arg Lys Gln Gly Val Ile Lys Leu Lys Asn Asn Gly		
385	390	395 400
Asp Phe Phe Ile Ala Asn Glu Gly Arg Arg Pro Ile Tyr Ile Asp Gly		
405	410	415

Arg Pro Val Leu Cys Gly Ser Lys Trp Arg Leu Ser Asn Asn Ser Val
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Val Glu Ile Ala Ser Leu Arg Phe Val Phe Leu Ile Asn Gln Asp Leu
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<210> 9

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
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<210> 10

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: polynucleotide

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<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polynucleotide

<400> 11

56

(The following are the names of the persons who have been appointed to the various committees of the Board of Directors, as shown on the preceding page.)